

# Package ‘hetsurrSurv’

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**Type** Package

**Title** Assessing Heterogeneity in Surrogacy Using Censored Data

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**Description** Provides functions to assess and test for heterogeneity in the utility of a surrogate marker with respect to a baseline covariate using censored (survival data), and to test for heterogeneity across multiple time points. More details will be available in the future in: Parast, L., Tian L, Cai, T. (2023) ``Assessing Heterogeneity in Surrogacy Using Censored Data." Under Review.

**License** GPL

**Imports** stats, Rsurrogate, MASS, groc

**NeedsCompilation** no

**Depends** R (>= 3.5.0)

## R topics documented:

example.data	1
R.main.estimate	2
test.multiplet	4

<b>Index</b>	<b>6</b>
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example.data	<i>Example data</i>
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## Description

Example data

## Usage

```
data("example.data")
```

## Format

A list with 10 elements representing 2000 observations from a treatment group and 1500 observations from a control group:

s1 the surrogate marker in the treatment group  
 s0 the surrogate marker in the control group  
 w1 the baseline covariate of interest in the treatment group  
 w0 the baseline covariate of interest in the control group  
 d1 the event indicator in the treatment group  
 d0 the event indicator in the control group  
 x1 the observed event time in the treatment group  
 x0 the observed event time in the control group  
 w1\_cat the discrete baseline covariate of interest in the treatment group  
 w0\_cat the discrete baseline covariate of interest in the control group

## Examples

```
data(example.data)
names(example.data)
```

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R.main.estimate	<i>Estimates the proportion of treatment effect explained by the surrogate marker as a function of a baseline covariate</i>
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## Description

Assesses heterogeneity in the utility of a surrogate marker with respect to a baseline covariate using censored (survival data) by estimates the proportion of treatment effect explained by the surrogate marker as a function of a baseline covariate, w

## Usage

```
R.main.estimate(xone, xzero, deltaone, deltazero, sone, szero, wone, wzero, w.grd, myt,
landmark, type = "cont", var = FALSE, test = FALSE, extrapolate = T, h.0 = NULL,
h.1 = NULL, h.w = NULL, h.s = NULL, h.w.1 = NULL)
```

## Arguments

xone	x1, observed event time in the treated group
xzero	x0, observed event time in the control group
deltaone	delta1, event indicator in the treated group
deltazero	delta0, event indicator in the control group
sone	s1, surrogate marker in the treated group
szero	s0, surrogate marker in the control group
wone	w1, baseline covariate in the treated group
wzero	w0, baseline covariate in the control group

w.grd	grid for w where estimation will be provided
myt	t of interest
landmark	t0, landmark time
type	options are "cont" or "discrete"; type of baseline covariate, default is "cont"
var	TRUE or FALSE, if variance/standard error estimates are wanted
test	TRUE or FALSE, if test for heterogeneity is wanted
extrapolate	TRUE or FALSE
h.0	bandwidth
h.1	bandwidth
h.w	bandwidth
h.s	bandwidth
h.w.1	bandwidth

### Value

A list is returned:

w.values	grid for w where estimation is provided
R.s.w	The proportion of treatment effect explained as a function of the baseline covariate, w
delta.w	The treatment effect as a function of the baseline covariate, w
delta.s.w	The residual treatment effect as a function of the baseline covariate, w
sd.R	Standard error estimate of R.s.w
sd.delta	Standard error estimate of delta.w
sd.delta.s	Standard error estimate of delta.s.w
pval.omnibus	p-value from the omnibus test for heterogeneity
pval.con	p-value from the conservative omnibus test for heterogeneity

### Author(s)

Layla Parast

### References

Parast, L., Tian L, Cai, T. (2023) "Assessing Heterogeneity in Surrogacy Using Censored Data." Under Review.

### Examples

```
data(example.data)
names(example.data)
R.main.estimate(xone=example.data$x1, xzero=example.data$x0, deltaone=example.data$d1,
deltazero=example.data$d0, sone=log(example.data$s1), szero=log(example.data$s0),
wone=log(example.data$w1), wzero=log(example.data$w0),
w.grd=log(seq(0.1,0.9, length=25)), myt=1, landmark=0.5)
R.main.estimate(xone=example.data$x1, xzero=example.data$x0, deltaone=example.data$d1,
deltazero=example.data$d0, sone=log(example.data$s1), szero=log(example.data$s0),
wone=example.data$w1_cat, wzero=example.data$w0_cat,
myt=1, landmark=0.5,type = "discrete", w.grd = c(1,2,3,4))
```

```
#computationally intensive
```

```
R.main.estimate(xone=example.data$x1, xzero=example.data$x0, deltaone=example.data$d1,
deltazero=example.data$d0, sone=log(example.data$s1), szero=log(example.data$s0),
wone=log(example.data$w1), wzero=log(example.data$w0),
w.grd=log(seq(0.1,0.9, length=25)), myt=1, landmark=0.5, test=TRUE)
```

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test.multiplet

*Tests for heterogeneity across multiple timepoints*


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## Description

Tests for heterogeneity across multiple timepoints

## Usage

```
test.multiplet(t.mult, xone, xzero, deltaone, deltazero, sone, szero, wone,
wzero, w.grd, landmark, extrapolate = T, h.0 = NULL, h.1 = NULL, h.w = NULL,
h.s = NULL, h.w.1 = NULL, type = "cont")
```

## Arguments

t.mult	Vector of time points
xone	x1, observed event time in the treated group
xzero	x0, observed event time in the control group
deltaone	delta1, event indicator in the treated group
deltazero	delta0, event indicator in the control group
sone	s1, surrogate marker in the treated group
szero	s0, surrogate marker in the control group
wone	w1, baseline covariate in the treated group
wzero	w0, baseline covariate in the control group
w.grd	grid for w where estimation will be provided
landmark	t0, landmark time
extrapolate	TRUE or FALSE
h.0	bandwidth
h.1	bandwidth
h.w	bandwidth
h.s	bandwidth
h.w.1	bandwidth
type	options are "cont" or "discrete"; type of baseline covariate, default is "cont"

## Value

A list is returned:

pval.multi	p-value for omnibus test
pval.con.multi	p-value for conservative omnibus test (only applicable for continuous W)

**Author(s)**

Layla Parast

**References**

Parast, L., Tian L, Cai, T. (2023) "Assessing Heterogeneity in Surrogacy Using Censored Data." Under Review.

**Examples**

```
data(example.data)
names(example.data)
#computationally intensive

test.multiplet(t.mult = c(1,1.25,1.5), xone=example.data$x1, xzero=example.data$x0,
deltaone=example.data$d1, deltazero=example.data$d0, sone=log(example.data$s1),
szero=log(example.data$s0), wone=log(example.data$w1), wzero=log(example.data$w0),
w.grd=log(seq(0.1,0.9, length=25)), landmark=0.5)
```

# Index

`example.data`, [1](#)

`R.main.estimate`, [2](#)

`test.multiplet`, [4](#)